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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Sharron G. Penn et al.
Serial No. : 09/774,203
Conf. No. : 7320
Filed: : January 29, 2001
For: : METHODS AND APPARATUS FOR PREDICTING,
CONFIRMING, AND DISPLAYING FUNCTIONAL
INFORMATION DERIVED FROM GENOMIC
SEQUENCE

Group Art Unit : 1645

Hon. Commissioner for Patents
Washington, D.C. 20231

SECOND SUPPLEMENTAL INFORMATION DISCLOSURE STATEMENT

Sir:

Pursuant to 37 C.F.R. §§ 1.56, 1.97 and 1.98,
applicants hereby make the following documents of record in
the above identified application:
*

Other Documents

Adams, M.D. et al. Initial assessment of human gene
diversity and expression patterns based upon 83 million
nucleotides of cDNA sequence. Nature 377, 3-174 (1995).

Adams, M.D. et al. The genome sequence of Drosophila
melanogaster. Science 287, 2185-2195 (2000).

* Applicants reserve the right to challenge the status of
any of the cited documents as prior art.

Altschul, S.F. et al. Basic local alignment search tool. J. Mol. Biol. 215, 403-410 (1990).

Batzoglou, S., Pachter, L., Mesirov, J. P., Berger, B. & Lander, E. S. Human and mouse gene structure: comparative analysis and application to exon prediction. Genome Res. 10, 950-958 (2000).

Black, D. L. Protein diversity from alternative splicing: a challenge for bioinformatics and post-genome biology. Cell 103, 367-370 (2000).

Brett, D. et al. EST comparison indicates 38% of human mRNAs contain possible alternative splice forms. FEBS Lett. 474, 83-86 (2000).

Boguski, M. S. Biosequence exegesis. Science 286, 453-455 (1999).

Claverie, J. M. Computational methods for the identification of genes in vertebrate genomic sequences. Hum. Mol. Genet. 6, 1735-1744 (1997).

de Souza, S. J. et al. Identification of human chromosome 22 transcribed sequences with ORF expressed sequence tags. Proc. Natl Acad. Sci. USA 97, 12690-12693 (2000).

Ewing, B. & Green, P. Analysis of expressed sequence tags indicates 35,000 human genes. Nature Genet. 25, 232-234 (2000).

Guigo, R., Agarwal, P., Abril, J. F., Burset, M. & Fickett, J. W. An assessment of gene prediction accuracy in large DNA sequences. Genome Res. 10, 1631-1642 (2000).

Hanke, J. et al. Alternative splicing of human genes: more the rule than the exception? Trends Genet. 15, 389-390 (1999).

Hubbard, T. & Birney, E. Open annotation offers a democratic solution to genome sequencing. Nature 403, 825 (2000).

Hughes, T. R. et al. Functional discovery via a compendium of expression profiles. Cell 102, 109-126 (2000).

Liang, F. et al. Gene index analysis of the human genome estimates approximately 120,000 genes. Nature Genet. 25, 239-240 (2000).

- Makalowski, W. & Boguski, M. S. Evolutionary parameters of the transcribed mammalian genome: an analysis of 2,820 orthologous rodent and human sequences. *Proc. Natl Acad. Sci. USA* 95, 9407-9412 (1998).
- Marshall, E. Public-private project to deliver mouse genome in 6 months. *Science* 290, 242-243 (2000).
- Blanchard, A. P., Kaiser, R. J. & Hood, L. E. High-density oligonucleotide arrays. *Biosens. Bioelectron.* 6/7, 687-690 (1996).
- Marton, M. J. *et al.* Drug target validation and identification of secondary drug target effects using DNA microarrays. *Nature Med.* 4, 1293-1301 (1998).
- Mironov, A. A., Fickett, J. W. & Gelfand, M. S. Frequent alternative splicing of human genes. *Genome Res.* 9, 1288-1293 (1999).
- The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNAs collection. *Nature* 409, 685-690 (2001).
- Roberts, C. J. *et al.* Signaling and circuitry of multiple MAPK pathways revealed by a matrix of global gene expression profiles. *Science* 287, 873-880 (2000).
- Roest Crolius, H. *et al.* Estimate of human gene number provided by genome-wide analysis using *Tetraodon nigroviridis* DNA sequence. *Nature Genet.* 25, 235-238 (2000).
- Rubin, G. M. *et al.* Comparative genomics of the eukaryotes. *Science* 287, 2204-2215 (2000).
- Strausberg, R. L., Feingold, E. A., Klausner, R. D. & Collins, F. S. The mammalian gene collection. *Science* 286, 455-457 (1999).
- Ullrich, B. *et al.* Functional properties of multiple synaptotagmins in brain. *Neuron* 13(6): 1281-1291 (1994).
- Wheelan, S. J. & Boguski, M. S. Late-night thoughts on the sequence annotation problem. *Genome Res.* 8, 168-169 (1998).
- Wigge, P. & McMahon, H.T. The amphiphysin family of proteins and their role in endocytosis at the synapse. *Trends Neurosci.* 21, 339-344 (1998).

Worley, J. et al. "A systems approach to fabricating and analyzing DNA microarrays," in Microarray Biochip Technology (ed. Schena, M.) 65-86 (Biotechniques Books, Natick, Massachusetts, 2000).

Copies of the aforementioned documents, which are listed on the accompanying Form PTO-1449 (submitted in duplicate), are enclosed herewith.

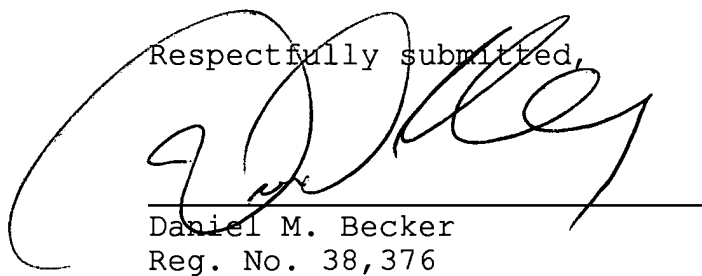
It is respectfully requested that this document be (1) fully considered by the Patent and Trademark Office during the examination of this application; and (2) printed on any patent that may issue on this application.

Applicants request that a copy of Form PTO-1449 (submitted in duplicate herewith), as considered and initialed by the Examiner, be returned with the next communication.

An early and favorable action is respectfully requested.

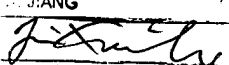
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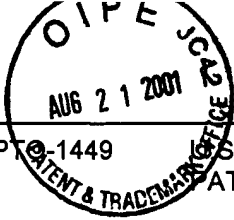
Respectfully submitted,


Daniel M. Becker
Reg. No. 38,376
Attorney for Applicants

FISH & NEAVE
Customer No. 1473
1251 Avenue of the Americas
New York, N. Y. 10020
(650) 617-4000 (CA)

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09/774,203INFORMATION DISCLOSURE
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Penn et al.FILING DATE
January 29, 2001CLASS
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U.S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS	FILING DATE IF APPROPRIATE

FOREIGN PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUBCLASS	TRANSLATION	
						YES	NO

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.)

EXAMINER INITIAL	
	Adams, M.D. et al. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence. <i>Nature</i> 377, 3-174 (1995).
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